

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/541,626
Source: IFWJ0
Date Processed by STIC: 4/29/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/541,626

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/541,626

DATE: 04/27/2006

TIME: 09:14:14

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04272006\J541626.raw

*many lines
Speed 72
character.*

3 <110> APPLICANT: Haruo HANAWA
5 <120> TITLE OF INVENTION: VECTOR FOR GENE THERAPY AND METHOD OF QUANTIFYING
TARGET PROTEIN IN

6 MAMMAL OR CULTURED CELLS WITH THE ADMINISTRATION OF THE VECTOR FOR
GENE

7 THERAPY

9 <130> FILE REFERENCE: 0760-0347PUS1

11 <140> CURRENT APPLICATION NUMBER: US 10/541,626

12 <141> CURRENT FILING DATE: 2005-07-07

14 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/016956

15 <151> PRIOR FILING DATE: 2003-12-26

17 <150> PRIOR APPLICATION NUMBER: JP 2003-3967

18 <151> PRIOR FILING DATE: 2003-01-10

20 <160> NUMBER OF SEQ ID NOS: 24

22 <210> SEQ ID NO: 1

23 <211> LENGTH: 11

24 <212> TYPE: PRT

25 <213> ORGANISM: Artificial Sequence

27 <220> FEATURE:

28 <223> OTHER INFORMATION: oligopeptide encoding C19-29 region of glucagon of
human, mouse or rat

30 <400> SEQUENCE: 1

32 Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr

33 1 5 10

36 <210> SEQ ID NO: 2

37 <211> LENGTH: 1471

38 <212> TYPE: DNA

39 <213> ORGANISM: Artificial Sequence

41 <220> FEATURE:

42 <223> OTHER INFORMATION: DNA insert encoding rat IFN-r receptor, rat IgG Fc
region and glucagon

43 C19-29 region

46 <220> FEATURE:

47 <221> NAME/KEY: CDS

48 <222> LOCATION: (13)..(1461)

49 <223> OTHER INFORMATION: DNA insert encoding rat IFN-r receptor, rat IgG Fc
region and glucagon

50 C19-29 region

52 <400> SEQUENCE: 2

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54 Met Ile Leu Leu Val Val Leu Met Leu Ser Ala Glu Ile

55 1 5 10

57 ggg agt gga gct ttg atg agc acc gag gat cct aag ccg ccc tcg gtg 99

58 Gly Ser Gly Ala Leu Met Ser Thr Glu Asp Pro Lys Pro Pro Ser Val

pp 1, 7
**Does Not Comply
Corrected Diskette Needed**

*this
is a
DNA
function*

*see
on Euro
summary
sheet.
Please
correct
this
throughout
file.*

59	15					20					25								
61	cct	gcg	cca	aca	aat	gtt	cta	att	acg	tcc	tat	gac	ttg	aac	cct	gtc			147
62	Pro	Ala	Pro	Thr	Asn	Val	Leu	Ile	Thr	Ser	Tyr	Asp	Leu	Asn	Pro	Val			
63	30					35					40					45			

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67	50 55 60	
69	cag gta aag atg tat cca gaa tac tgg act gat gcc tgc acc aac att	243
70	Gln Val Lys Met Tyr Pro Glu Tyr Trp Thr Asp Ala Cys Thr Asn Ile	
71	65 70 75	
73	gcc cat cat tat tgt aat atc tac aaa cac att tcc tat cct gac tca	291
74	Ala His His Tyr Cys Asn Ile Tyr Lys His Ile Ser Tyr Pro Asp Ser	
75	80 85 90	
77	tct gcc tgg gcc aga gtt aag gcc aag gtt gga caa aga gaa tct gcc	339
78	Ser Ala Trp Ala Arg Val Lys Ala Lys Val Gly Gln Arg Glu Ser Ala	
79	95 100 105	
81	tat gcg cag tca gaa gag ttt att atg tgc cga aag ggg aag gtt gga	387
82	Tyr Ala Gln Ser Glu Glu Phe Ile Met Cys Arg Lys Gly Lys Val Gly	
83	110 115 120 125	
85	ccg cct ggc ctg gac atc gga agg aag gaa gat cag ctg att gtc cac	435
86	Pro Pro Gly Leu Asp Ile Gly Arg Lys Glu Asp Gln Leu Ile Val His	
87	130 135 140	
89	ata ttt cac cct aag gtc aat gtg agt cag gaa acc atg ttt ggt gac	483
90	Ile Phe His Pro Lys Val Asn Val Ser Gln Glu Thr Met Phe Gly Asp	
91	145 150 155	
93	gga aat acc tgt tac aca ttc gac tac act gtg ttt gtg aaa cat tac	531
94	Gly Asn Thr Cys Tyr Thr Phe Asp Tyr Thr Val Phe Val Lys His Tyr	
95	160 165 170	
97	agg agt ggg gag atc cta cat aca gaa cat agc gtc cta aaa gaa gat	579
98	Arg Ser Gly Glu Ile Leu His Thr Glu His Ser Val Leu Lys Glu Asp	
99	175 180 185	
101	tgt agc gaa act ctg tgt gag tta aac atc tca gtg tcc acg ctg aat	627
102	Cys Ser Glu Thr Leu Cys Glu Leu Asn Ile Ser Val Ser Thr Leu Asn	
103	190 195 200 205	
105	tcc aat tac tgt gtt tca gta gtt gga aag tgc tct ttc tgg caa gtt	675
106	Ser Asn Tyr Cys Val Ser Val Val Gly Lys Ser Ser Phe Trp Gln Val	
107	210 215 220	
109	aat aca gaa aca tca aaa gac gcc tgt atc ccc ttt ctc cat gat gac	723
110	Asn Thr Glu Thr Ser Lys Asp Ala Cys Ile Pro Phe Leu His Asp Asp	
111	225 230 235	
113	aga gaa gaa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc aag	771
114	Arg Glu Glu Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys Lys	
115	240 245 250	
117	cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc ccc	819
118	Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe Pro	
119	255 260 265	
121	cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc acg	867
122	Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr	
123	270 275 280 285	
125	tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc agc	915
126	Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe Ser	
127	290 295 300	
129	tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca cca	963

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131          305          310          315
133 gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc atc      1011
134 Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
135          320          325          330
137 ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc acc      1059
138 Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val Thr
139          335          340          345
141 agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc gaa      1107
142 Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Glu
143 350          355          360          365
145 ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag gaa      1155
146 Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys Glu
147          370          375          380
149 gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc ttc      1203
150 Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly Phe
151          385          390          395
153 tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca cag      1251
154 Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro Gln
155          400          405          410
157 gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt tac      1299
158 Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser Tyr
159          415          420          425
161 ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag gga      1347
162 Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln Gly
163 430          435          440          445
165 aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac cat      1395
166 Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
167          450          455          460
169 act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt gtg      1443
170 Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe Val
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173 cag tgg ttg atg aat acc tgagaattct      1471
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180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: DNA sequence of artificial expression vector

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pCAGGS

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191 ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag      180
193 ggactttcca ttgacgtcaa tgggtggact atttacggta aactgccac ttggcagtac      240
195 atcaagtgta tcatatgcc agtacgccc ctattgacgt caatgacggt aaatggccc      300
197 cctggcatta tgccagtac atgacctat gggactttcc tacttggcag tacatctacg      360
199 tattagtcac cgctattacc atgggtcgag gtgagcccca cgttctgctt cactctcccc      420

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Output Set: N:\CRF4\04272006\J541626.raw

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209	gggagtcgct	gcgttgccct	cgccccgtgc	cccgcctcgc	gccgcctcgc	gccgcccgc	720
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215	ccttaaagg	ctccgggagg	gccctttgtg	cgggggggag	cggtcgggg	ggtgctgctg	900
217	tgtgtgtgtg	cgtggggagc	gccgcgtgcg	gccgcgctg	cccggcggt	gtgagcgctg	960
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223	tgggggggtg	agcagggggg	gtgggcgcgg	cggtcgggct	gtaaccccc	cctgcacccc	1140
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227	gcggggctcg	ccgtgcgggg	cggggggtgg	cggcaggtgg	gggtgcgggg	cggggcgggg	1260
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251	ttttgtgtct	ctcactcgga	aggacatatg	ggagggcaaa	tcatttaaaa	catcagaatg	1980
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291	aagataccag	gcgtttcccc	ctggaagctc	cctcgtcgcg	tctcctgttc	cgaccctgcc	3180
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295	acgctgtagg	tatctcagtt	cgggtgtagg	cgttcgctcc	aagctgggct	gtgtgcacga	3300
297	acccccggt	cagccccgacc	gctgcgcctt	atccggtaac	tatcgtcttg	agtcacaacc	3360

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Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04272006\J541626.raw

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333 tatgcggcga ccgagttgct cttgcccggc gtcaatacgg gataataccg cgccacatag 4440
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341 aaagggaata agggcgacac ggaaatgttg aatactcata ctcttccttt ttcaatatta 4680
343 ttgaagcatt tatcagggtt attgtctcat gagcggatag atatttgaat gtatttagaa 4740
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348 <210> SEQ ID NO: 4

349 <211> LENGTH: 1233

350 <212> TYPE: DNA

351 <213> ORGANISM: Artificial Sequence

353 <220> FEATURE:

354 <223> OTHER INFORMATION: DNA insert encoding rat CTLA4, rat IgG Fc region
and glucagon C19-29

355 region

357 <220> FEATURE:

358 <221> NAME/KEY: CDS

359 <222> LOCATION: (13)..(1224)

360 <223> OTHER INFORMATION: DNA insert encoding rat CTLA4, rat IgG Fc region
and glucagon C19-29

361 region

363 <400> SEQUENCE: 4

364 gaattcattt aa atg gct tgt ctt gga ctc cag agg tac aaa act cac ctg 51

365 Met Ala Cys Leu Gly Leu Gln Arg Tyr Lys Thr His Leu

366 1 5 10

368 cag ctg cct tct agg act tgg cct ttt gga gtc ctg ctt tct ctt ctc 99

369 Gln Leu Pro Ser Arg Thr Trp Pro Phe Gly Val Leu Leu Ser Leu Leu

370 15 20 25

372 ttc atc cca atc ttc tct gaa gcc ata caa gtg acc caa cct tca gtg 147

373 Phe Ile Pro Ile Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val

374 30 35 40 45

376 gtg ttg gcc agc agc cac ggt gtc gcc agc ttt cca tgt gaa tat gca 195

377 Val Leu Ala Ser Ser His Gly Val Ala Ser Phe Pro Cys Glu Tyr Ala

378 50 55 60

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/541,626

DATE: 04/27/2006
TIME: 09:14:15

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04272006\J541626.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 846
Seq#:10; Line(s) 858
Seq#:11; Line(s) 870
Seq#:12; Line(s) 882
Seq#:23; Line(s) 1023
Seq#:24; Line(s) 1035

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/541,626

DATE: 04/27/2006

TIME: 09:14:15

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\04272006\J541626.raw